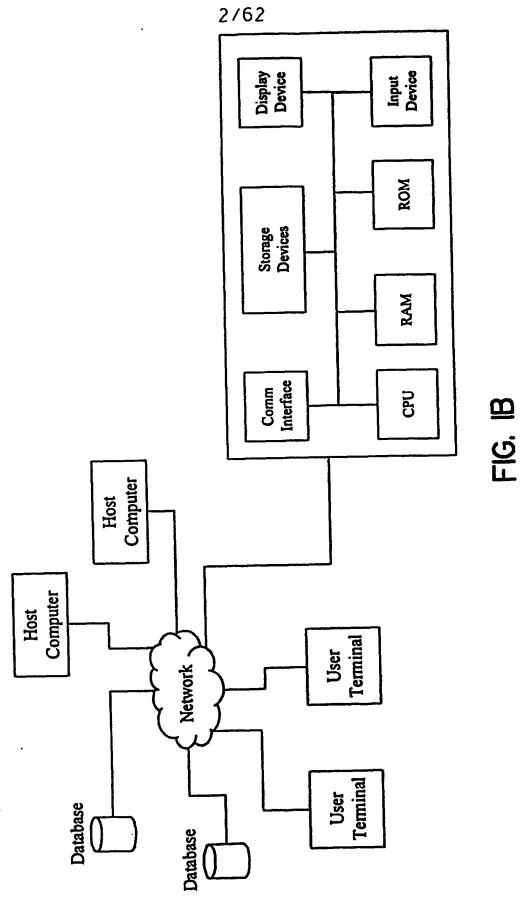
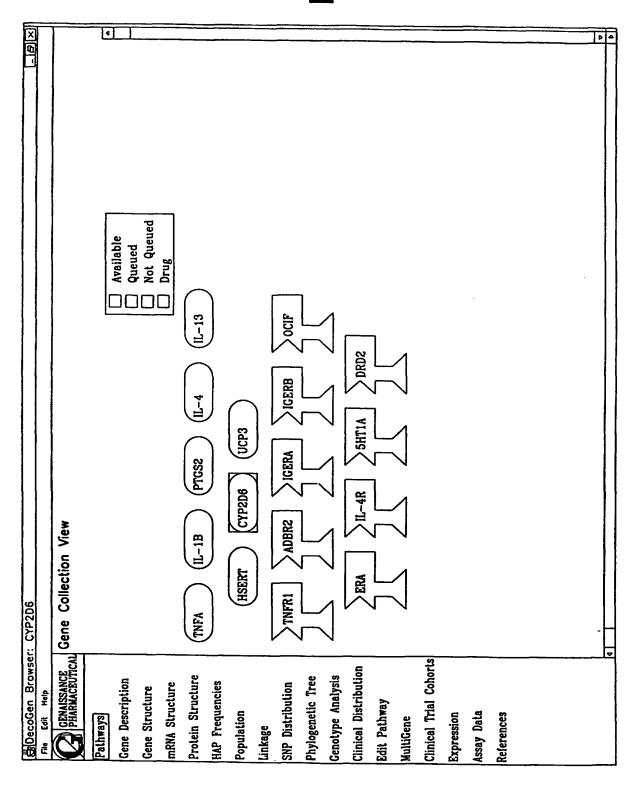


FIG. IA



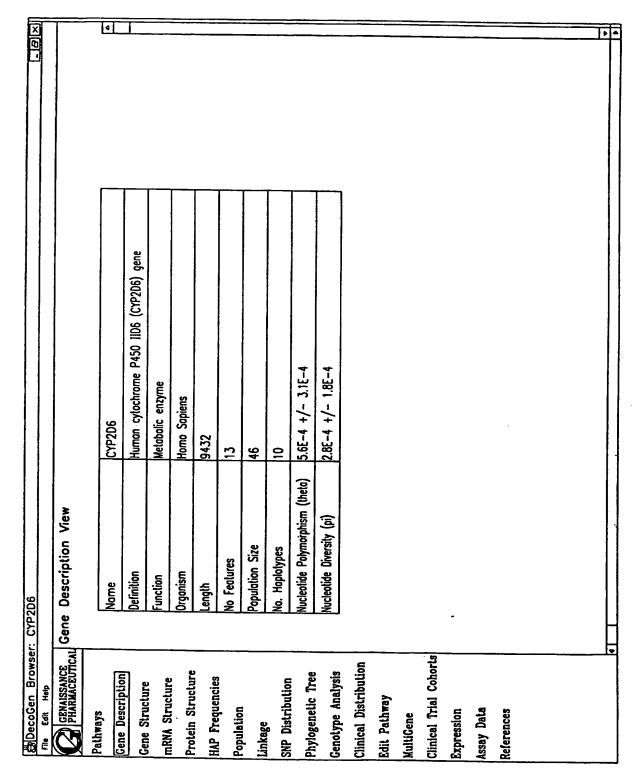
SUBSTITUTE SHEET (RULE 26)

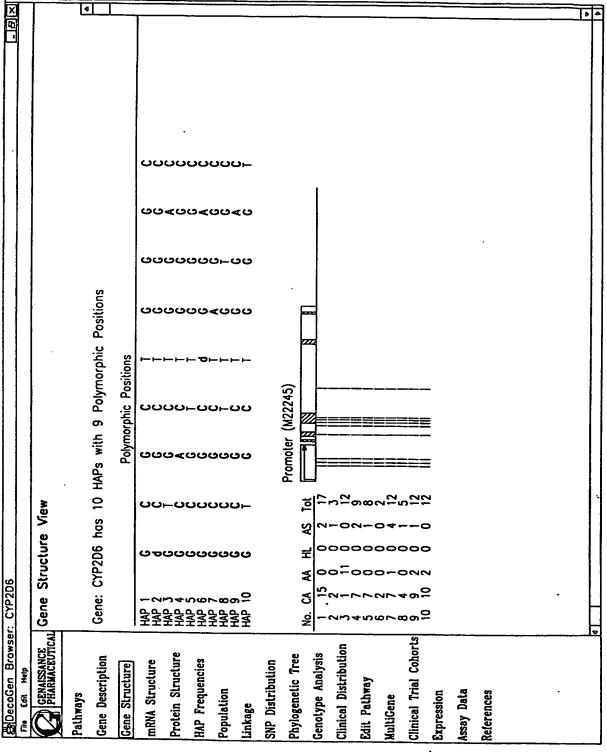
3/62 **(3**)



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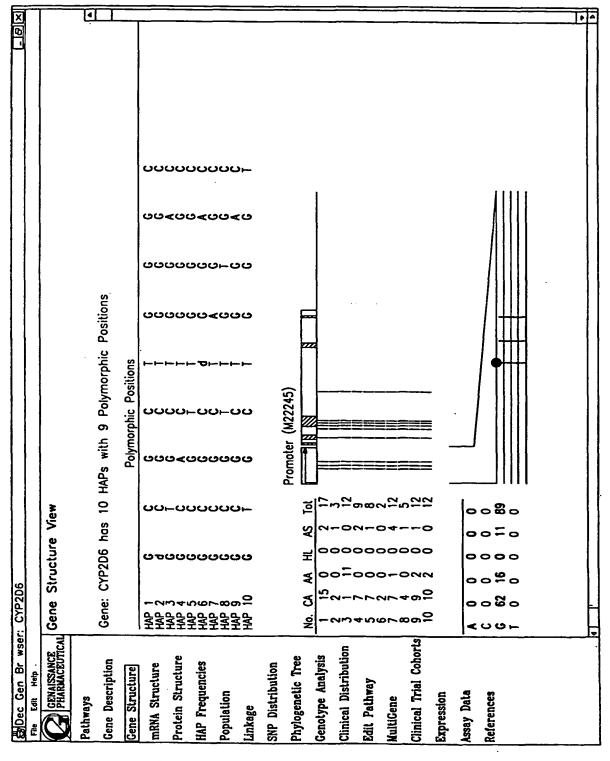
FIG. 3





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FIG. 4b (2)/9



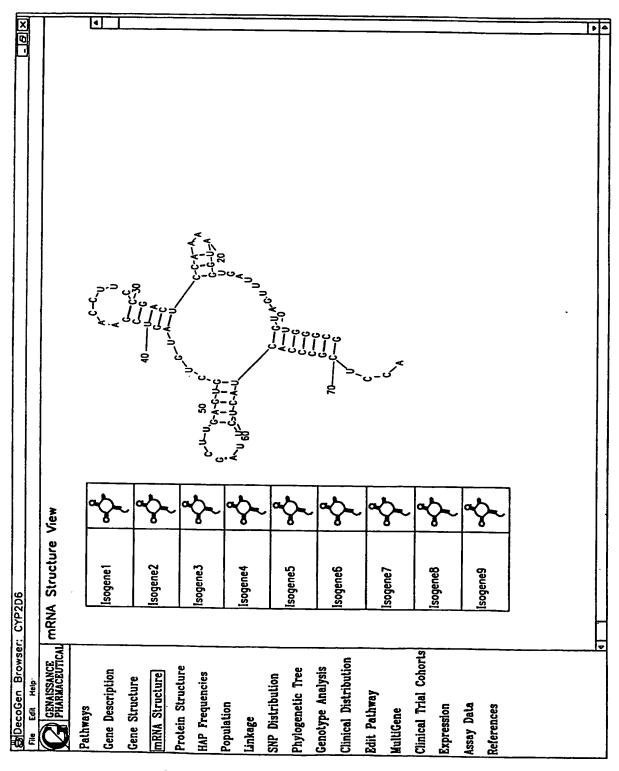
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388)		540	ototectgoo ototectgoo ototectgoo ototectgoo ototectgoo atotectgoo ototectgoo ototectgoo	
Gene (M33.		530	tacoogcoco tacoogcoco tacoogcoco tacoogcoco tacoogcoco tacoogcoco tacoogcoco tacoogcoco	
Alignment:	Colour Catculate Help	520		
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83	Ē		HAHAHAHAH HAHAHAHAH HAHAHAHAHAHAHAHAHAH	gone

FIG. 5

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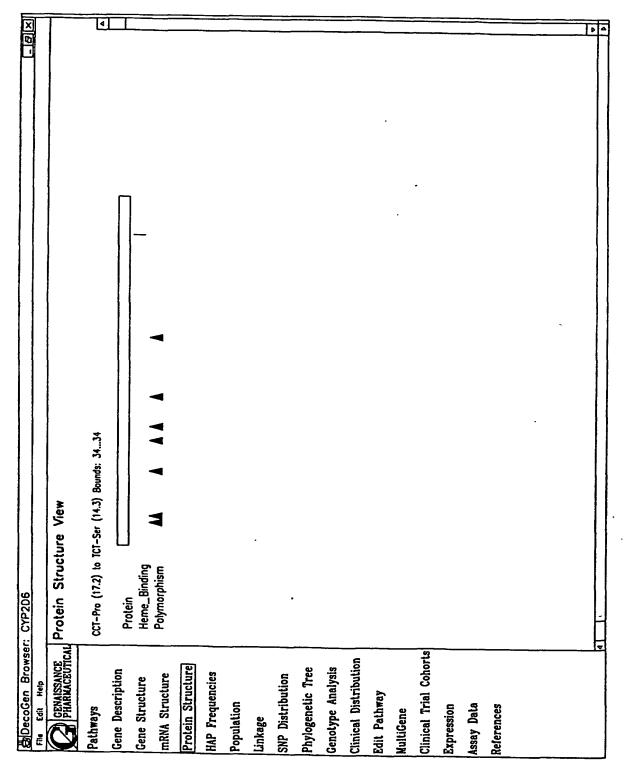
FIG.



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FIG.



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Blocogen Browser: CYP206	CYP206							- BX
File Edit Help.								
GENAISSANCE PHARMACEUTICAL	Population View	As						
Pathways	PID	Ethnicity	Age	Gender	HAP 1	HAP 2	Test	1
Gene Description	UP070	CA	66	Ŀ	GCCTGGC	GCCTGGC	0.1	
Gene Structure	UP072	క	66	Ŀ	decerecee	GCACTGGGC	0.2	
mRNA Structure	UP074	క	66	Ŀ	GCGCTGGGC	GCACTGGGC	0.2	
Protein Structure	UP132	CA	66	×	crectecer	crecreer	0.3	
HAP Frequencies	UP133	క	66	М	GCGCTGGGC	GTGCTGGGT	0.2	
Population	UP134	ς _γ	66	Ŀ	GCGCTGGGC	cccrcccc	0.1	
Linkage	UP137	ర	66	M	GTGCTGGGT	GTGCTGGGT	0.1	
SNP Distribution	UP009	ర	66	Į.	GCACTGGGC	GCACTGGGC	0.1	
Phylogenetic Tree	UP014	ర	66	<u>l</u> e.	deserteses	GCGCTGGAC	0.3	
Genotype Analysis	UP020	క	99	Ŀ	GTGCTGGGT	GTGCTGGGT	0.2	=
Clinical Distribution	UP021	ర	66	₹	ссеттетес	GCGCTGGGC	0.4	
Edit Pathway	UP022	క	66	≥	GCGCTGGAC	GCGCTGGAC	0.3	
MultiGene	OR001	AS	66	≥	deserteses	сстстсс	0.2	
Clinical Trial Cohorts	OR002	AS	66	> =	бсестевес	GCGCTGGGC	0.3	
Expression	OR004	AS	66	u.	GCACTGGGC	GCACTGGGC	0.2	
Assay Data	08006	γS	66	Ŀ	СССТГССС	GCGCTGGAC	0.1	
References	WT003	క	66	L	СССТСССС	ссеттетес	0.2	-
•	WT005	క	66	≥	ссеттесес	GCGCTGGGC	0.2	
	WT007	క	66	≥	СССТСТСС	ссеттетес	9.4	
	UP012	క	66	L.	GCGCTAGGC	GCCCTGCAC	0.1	
	UP135	ర	66	×	GCACTGGGC	GCCCTGGAC	0.2	Ī
								F

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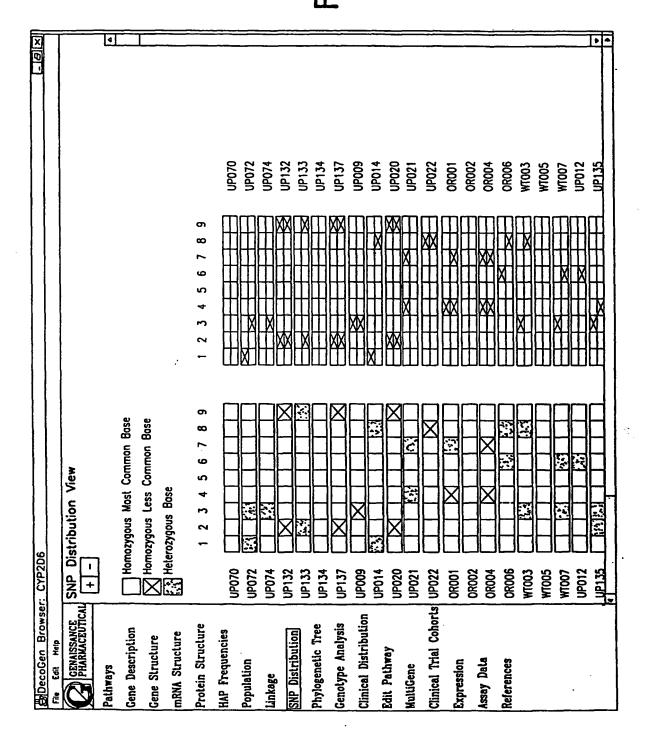
WO 01-01218 3/3

Date: 04 jan 2001

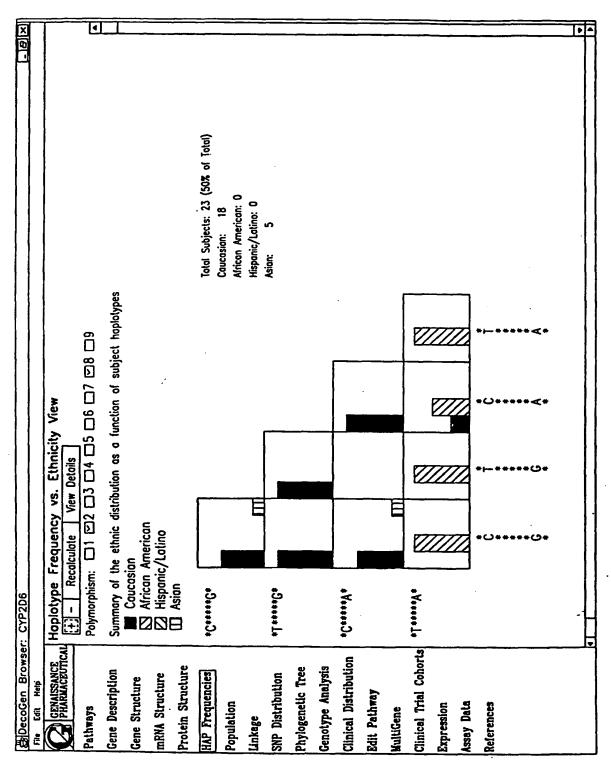
Destination: Agent

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F1G. 9

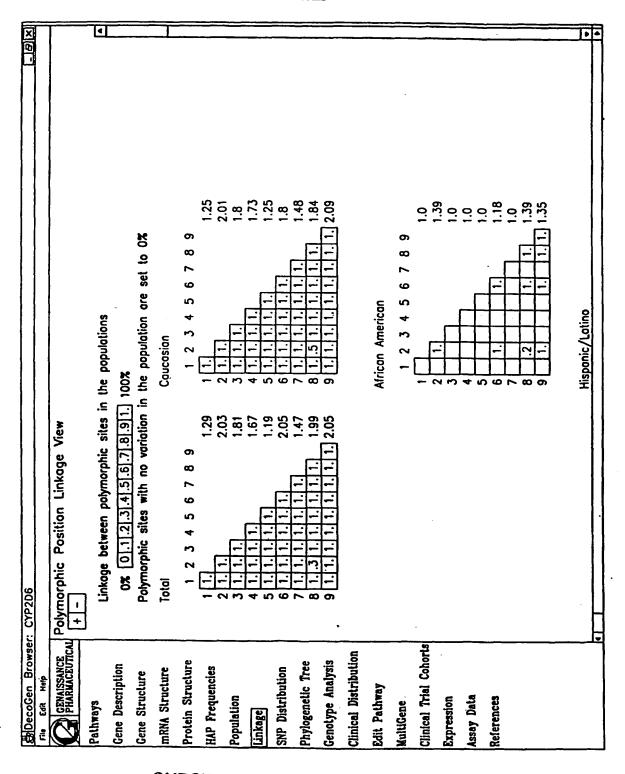


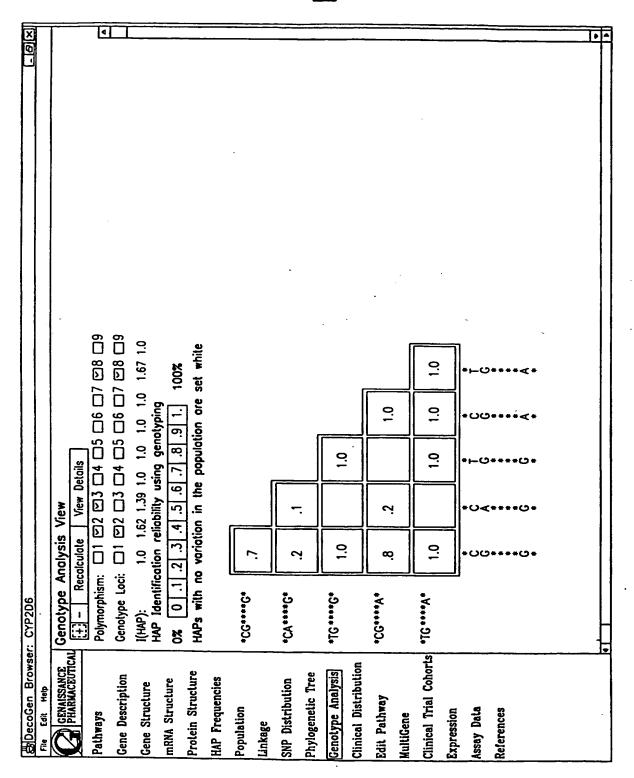
12 / 62 **Q 9**



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Bloecogen Browser: CY	: CYP206							- 16	Х <i>Ө</i> -
File Edit Help									
G GENAISSANCE PHARMACEUTICAL Pathways	Haplotype Frequer + - Recolculate Polymorphism: □1 €	Frequency vs. Ethnicity View scolculate [View Summary] 1; □1 ⊡2 □3 □4 □5 □6 □7 ⊡8 □9	, View	28 0					[
Gene Description	Details of the ethni	Details of the ethnic distribution as a function of subject haplotypes	tion of subj	ject hopl	otypes				
Gene Structure mRNA Structure	3 Columns ar Total numb	Columns are given for each Ethnogeographic group: Total number sampled with HAP pair	iogeographic g pair	Jroup:					
Protein Structure	Fraction of	Fraction of the ethnogeographic group with that HAP pair	roup with the	not HAP	pair				
HAP Frequencies	_	Aperica unider maray—ne HAP 2		2 60 20 20 20 20 20 20 20 20 20 20 20 20 20	Courresion	African American	Hispanir / oting		Ve.
Population	*D********	*0*******	23	50%	18 56.3% 37.9%	0 0.0% 0.6%	0 0.0%		ž
Linkage	*O*****L*	**************************************	7 4	8 % 8 %	2 6.3% 18.9% 4 12.5% 2.4%	0 0.0% 2.4%	0 0.0%	0.0%	
SNP Distribution	*C*****A*	*9******			12.5%	0.0%	0.0%		
Dhulosanstin Tree	*C*****	* V * * * * O *				0.0%	0.0%		
נוולוסקפוופרוכ זובב					0.0%	12.5%	0.0%		
Genotype Analysis	*V*****L*	* 🗸 * * * * • • • • • • • • • • • • • • •	7 M	4 % % %	0 0.0% 0.8% 1 3.1% 1.1%	2 25.0% 18.9% 2 25.0% 18.9%	0.0%	0.0%	
Clinical Distribution	*V*****L*	* V***** L*			_	37.5%	0.0%		
Edit Pathway									
MultiGene									
Clinical Trial Cohorts									
Expression									==
Assay Data					~				=
References									
					`				Ξ
								·	
_1.9									•
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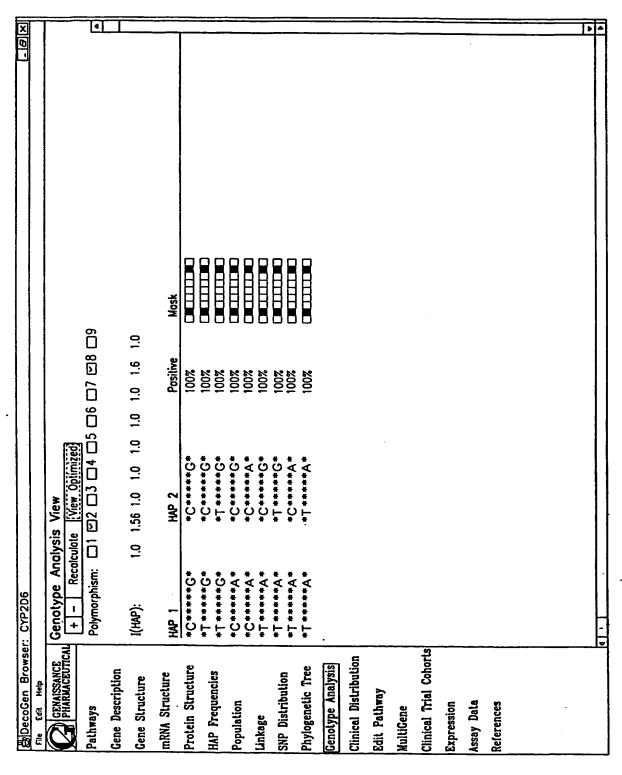
Bloec Gen Br wser: CYP	: CYP206				X
File Edit Help					i
GENAISSANCE PHARMACEUTICAL	Genotype Analysis View	s View [View Optimized]			<u> </u>
Pathways	Polymorphism: 1	13 04 0 5 0 6 1	- 1 전 8 대	٠	1
Gene Description		⊡2 □3 □4 □5 □6 C	口7 四8 口9	1_1	
Gene Structure	I(HAP): 1.0	1.56 1.0 1.0 1.0 1.0 1	1.0 1.6 1.0		
	HAP 1	HAP 2	X XPop.	Positive	
Protein Structure	*D*****O*	*9***		100%	
HAP Frequencies	******	******* ********	4 4%	100%	
	*V*****O*			2001	
Linkage	*C*****	* V * * * * * U *	5%	100%	
ribution	* V **** L *			100%	
	* V * * * * L *	_		100%	
Phylogenetic Tree	*V***** L*	****		100%	
Genotype Analysis					
Clinical Distribution	·				
Edit Pathway					_
MultiGene					
Clinical Trial Cohorts					
Expression					====
Assay Data					
References					===
					1
•					•

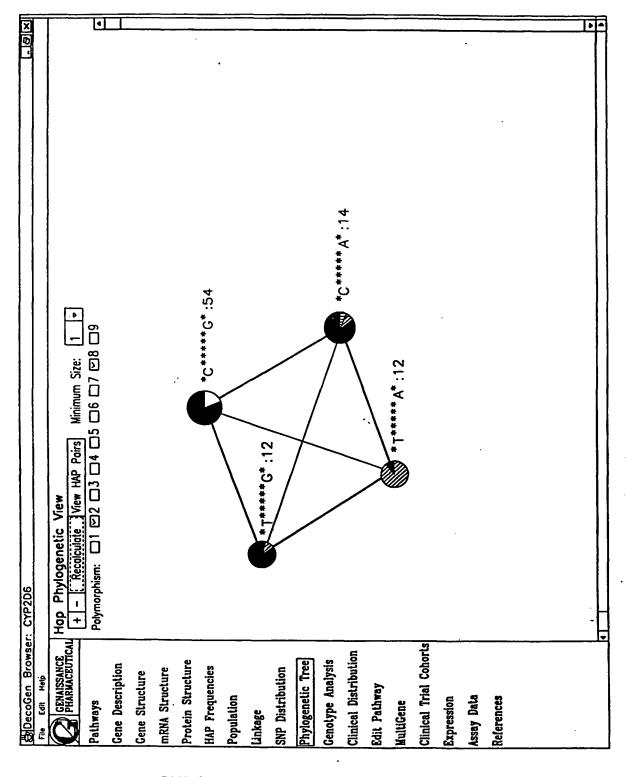
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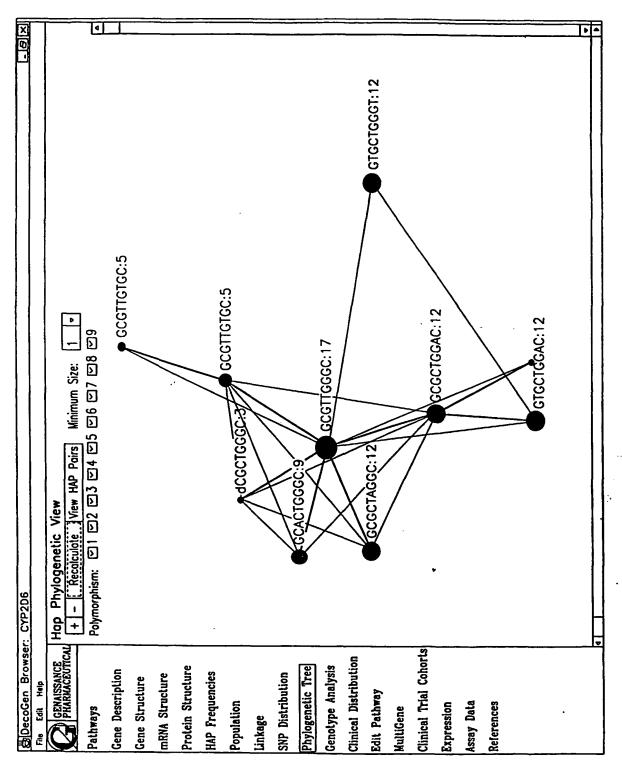
PCT/US00/17540

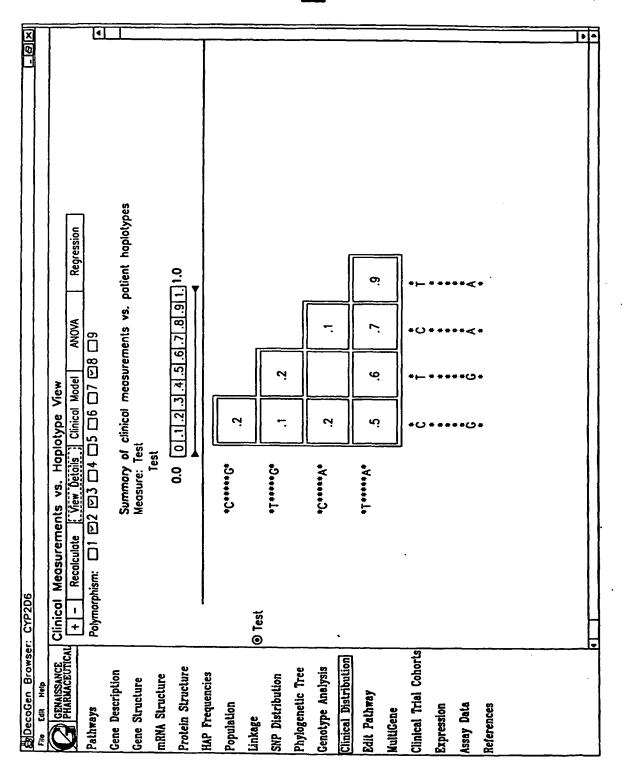
17 / 62 <u>9</u> <u>9</u>





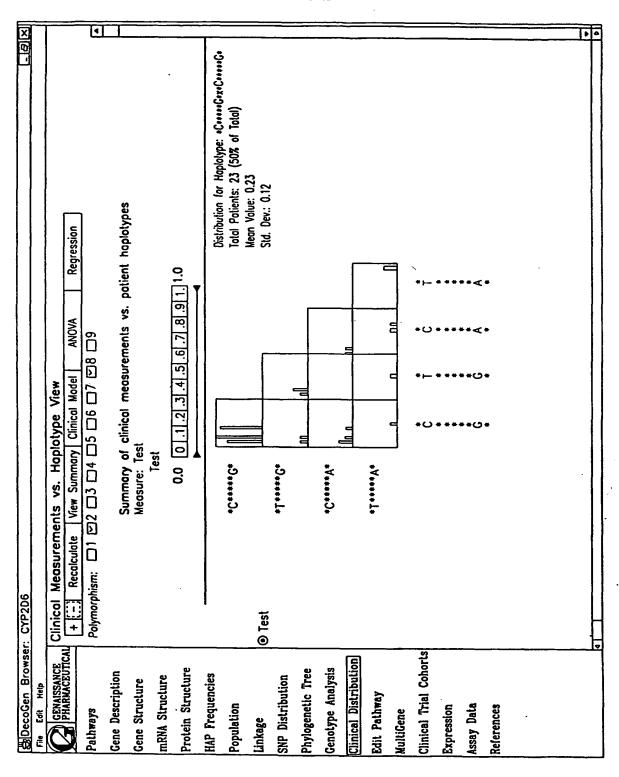
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FIG. 19



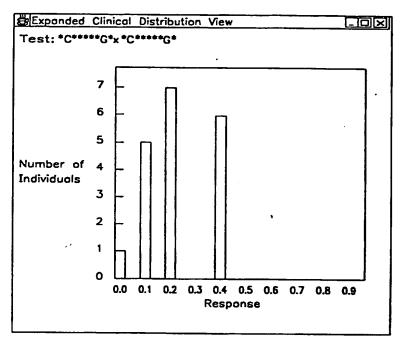


FIG. 20

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inical	Measure	ments Re	aression C	Calculation		
			J			
Site	Slope	Intercept	Vorionce	T(slope)	Significance Level	
1	-0.083	0.316	0.05	-0.59	0.7223	
2	0.154	0.231	0.04	4.22	0.9999	
3	-0.08	0.326	0.05	-1.16	0.8735	
4	-0.0080	0.313	0.06	-0.14	0.5572	
5	0.145	0.305	0.05	0.86	0.804	
5	-0.08	0.332	0.05	-1.24	0.8902	
7	0.0070	0.31	0.06	0.08	0.5303	
8	0.158	0.222	0.04	4.34	1.0	
9	-0.043	0.322	0.05	-0.76	0.7752	
		/				
					·	

FIG. 21

(書Dec Gen Browser: CYP2D6	r: CYP206								XIO -
File Edit Help									
GENAISSANCE PHARMACEUTICAL	Clinical								
		+ - recolculate New Usinguitory Unincol Model And Polymorphism:	11cal model ANUVA	L Kegi	regression				
Gene Description		Summory of clin Meneure: Test	Summary of clinical measurements vs. patient haplotypes	potient 1	haplotype	ري ون			
mRNA Structure		Test			-				
Protein Structure		1.10 0.0	.2] .3] .4] .5] .6] .7] .8]	0:1.10					
HAP Frequencies									
Population	⊙ Test	HWP 1	Hop 2	2	XPop.	Mean	Stddev X • 2	X2	0(X•2 K-3)
Linkage		*9**********	*5************	23	20%	0.24	0.12	9.17	_
SNP Distribution			*******	~ ~	4 0 % 1	0.15	0.07	0 0	_
Dhulosanetin Tree		*V*****O*	********	+ ഹ	10%	0.22	0.13	9 69	
and the second section of		*C*****	*C*****	٣	29	0.13	0.15	0.0	_
Genotype Analysis		*V*****L*	*S******	-	2%	0.5	0.0	0.0	_
Clinical Distribution		* V * * * * L *	*D*****L*	7	4 % 1	0.55	0.07	0.0	_
Edit Pathway		• V••••• L•	*T****A*	n 0	% % 9%	.b 0.93	0.0	0.0	0.1 0.1 0.1 0.1 0.1
MultiGene				,				!	
Clinical Trial Cohorts									
Expression									
Assay Data	⊙ Test		-						
References									

011-11	ANOVA Modeler	: Test		<u> </u>	
Clinical Med	osurements	ANOVA	Calculati	n	
+ - Rec	calculate				
Polymorphism:	: 🗆1 🖾2 🗀	13 🗆 4 🗅	⊃5 □6 ⊏	07 四8 □9	
Source of Va	riation DF	Mean Squar	es F-ratio		_ 🗖
Between Grou	ips 7	0.26	19.65		~ H
Within Groups	37	0.01	13.00		[]
Critical F-Dis	tribution Value 90	X: 1.88			_
Critical F-Dis	tribution Value 95	X : 2.26			[]
Critical F-Dis	tribution Value 99	% : 3.16			
Significant be	tween-group varia	tion at the	90% cofiden	ce level	
	tween-group varia				
Significant be	tween-group varia	tion at the	99% confide	nce level	11
					1 1
'HAP 1	HAP 2	N	Average		
HAP 1	HAP 2	N 23			_
			Average	Std. Dev.	_
•CessesCe	*C****C*	23	Average 0.23	Std. Dev.	_
sCessesCe sCessesCe	*L*****C*	23 2	Average 0.23 0.15	Std. Dev. 0.12 0.07	_
.C	*C******C* *L*****C* *C*****C*	23 2 5 4 2	0.23 0.15 0.22	Std. Dev. 0.12 0.07 0.13	_
eLessece eCessece eCessece eCessesCe	*1****** *C****** *1******C* *C*****C*	23 2 5 4 2 3	Average 0.23 0.15 0.22 0.2	Std. Dev. 0.12 0.07 0.13 0.08	_
*1*****Ce *1*****Ce *C*****Co *C*****Ce	*1******* *1******* *C******* *L******** *C*******	23 2 5 4 2	Average 0.23 0.15 0.22 0.2 0.55	Std. Dev. 0.12 0.07 0.13 0.08 0.07	
*C*****C* *L*****C* *C*****C* *C*****C* *C******C*	*CossosVo *LossosVo *CossosVo *LossosCo *LossosCo	23 2 5 4 2 3	Average 0.23 0.15 0.22 0.2 0.55 0.13	Std. Dev. 0.12 0.07 0.13 0.08 0.07 0.15	_
*C********* *L********* *L******** *C******* *C******* *C******	*Cossos Vo *Lossos Vo *Lossos Co *Cossos Vo *Lossos Co	23 2 5 4 2 3 3	Average 0.23 0.15 0.22 0.2 0.55 0.13 0.6	Std. Dev. 0.12 0.07 0.13 0.08 0.07 0.15 0.09	

FIG. 23

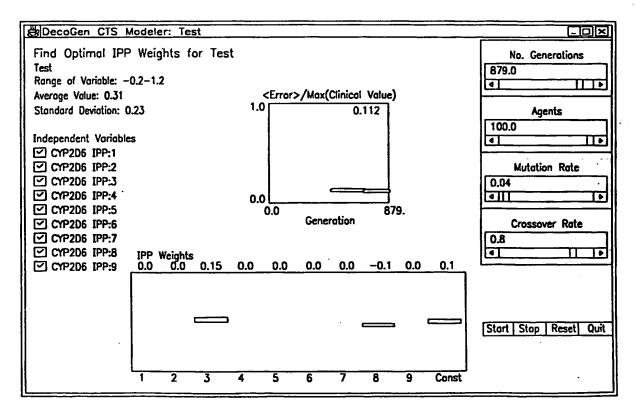
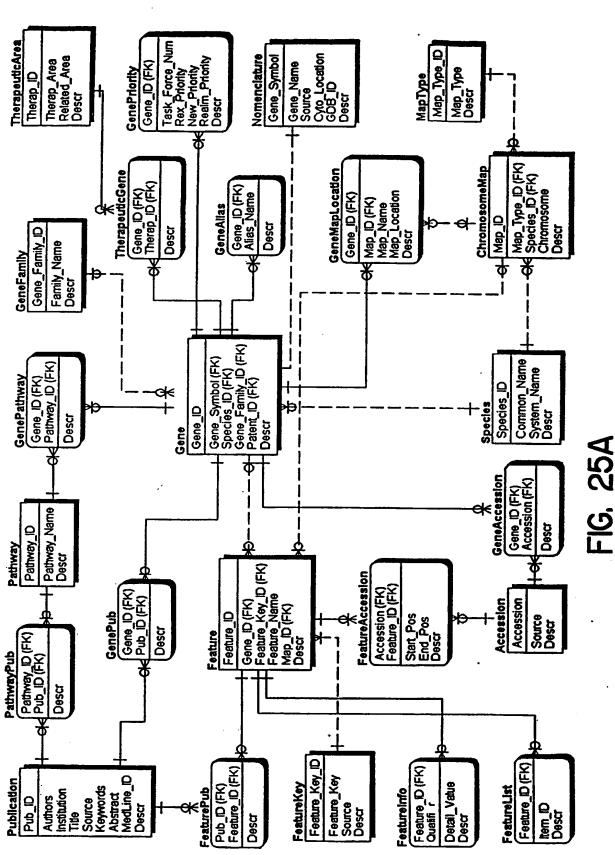
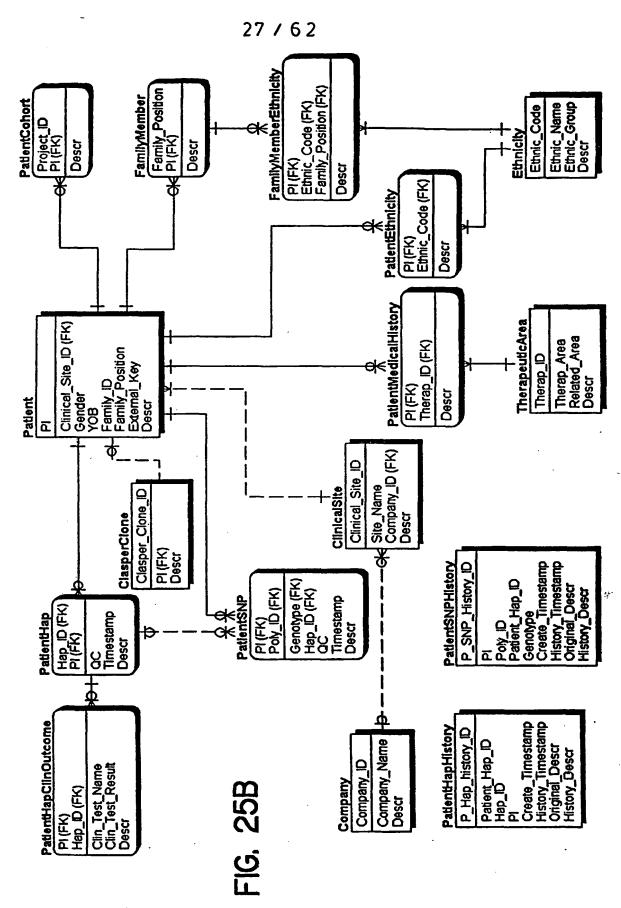


FIG. 24
SUBSTITUTE SHEET (RULE 26)



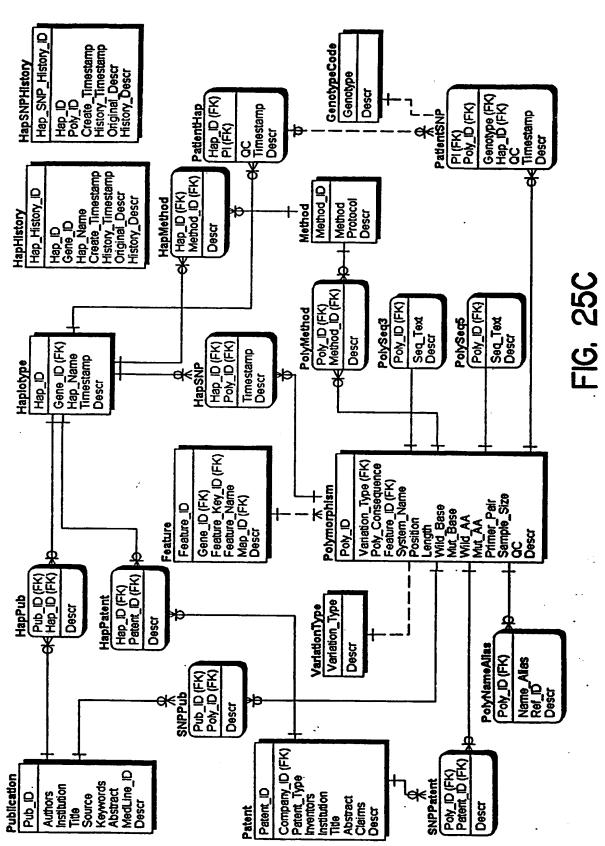


SUBSTITUTE SHEET (RULE 26)



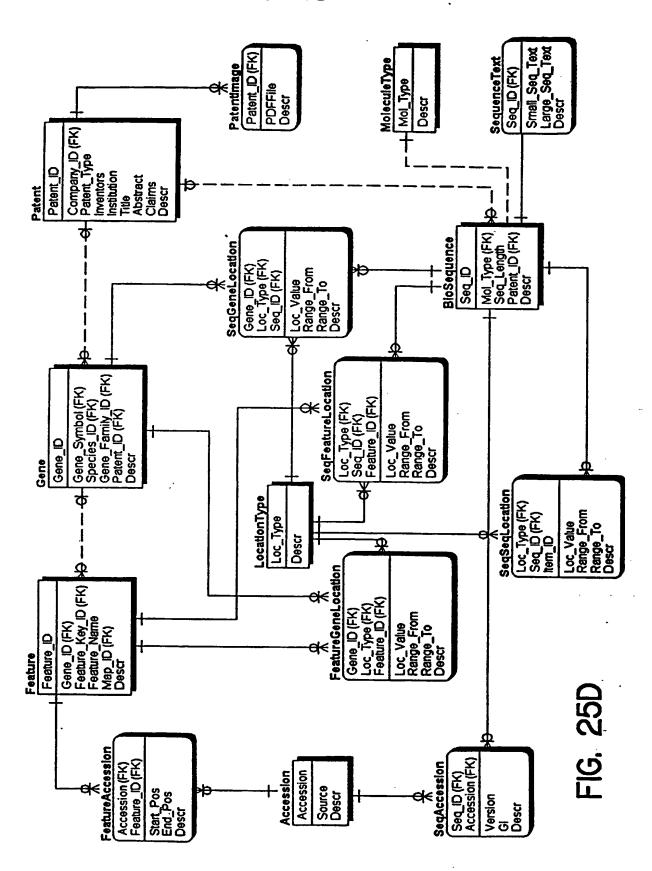
SUBSTITUTE SHEET (RULE 26)

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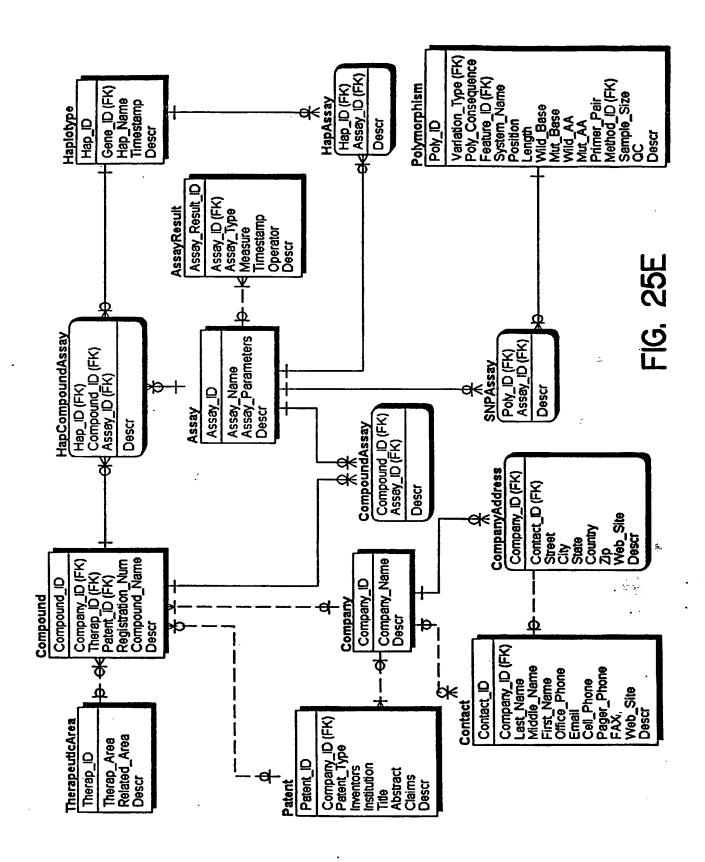


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SUBSTITUTE SHEET (RULE 26)

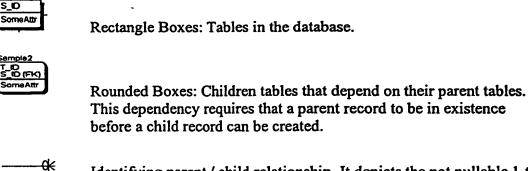


SUBSTITUTE SHEET (RULE 26)

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Legend of Figures:



- Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 10: |------ Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 14: \(\frac{1}{2} \frac{1}{2} \)
 Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

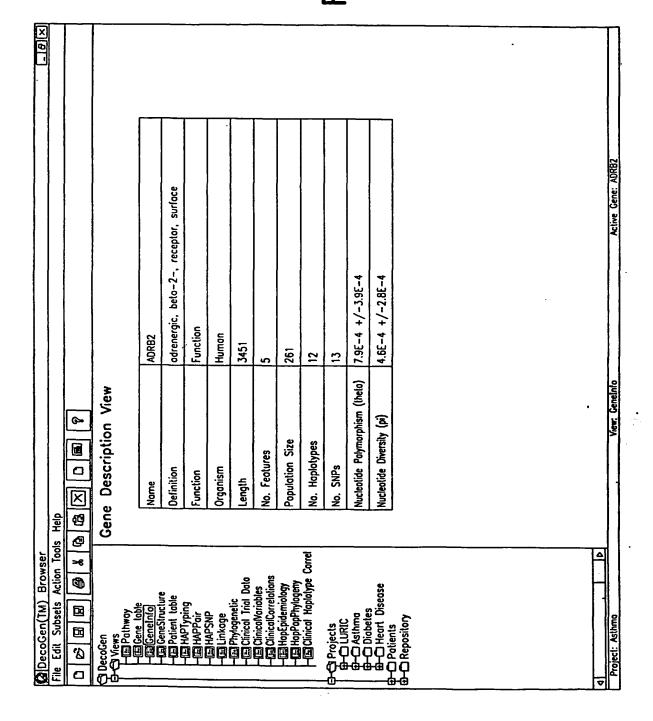
FIG. 25F

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FIG. 26

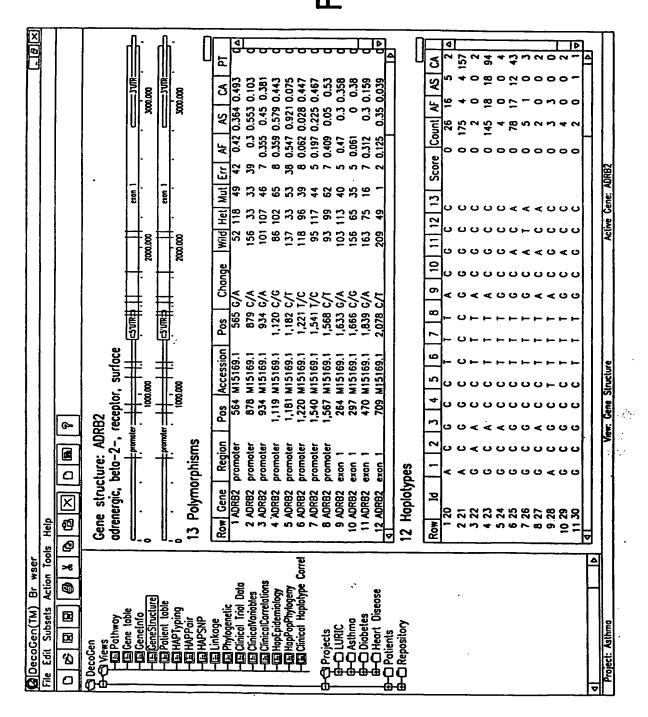
(A)DecoGen(TM) Browser	wser			×(6) =
File Edit Subsets Action Tools Help	on Tools Help			
		& © O		
CD Decoden CD Views ED Pathway ED Gene table ED GeneStructure ED Patient table ED HAPTyping ED HAPSNP ED Inkage ED Phydganetic ED Clinical Trial Data	Pathway View: Asthma	:w: Asthmo Extracellular OADBR2		
E ClinicalCorrelations E HapEpidemiology		Intracellular		
His Clinical Hapiotype Correl	Correi		OPDE68	Oils
PCProjects DC LURIC DC Diobetes DC Heart Disease DC Repository			OCALM1	O JAK3
4 Project: Asthmo		View: Politwoy	Active Gene: ADRB2	ADRB2
	•			

FIG. 27



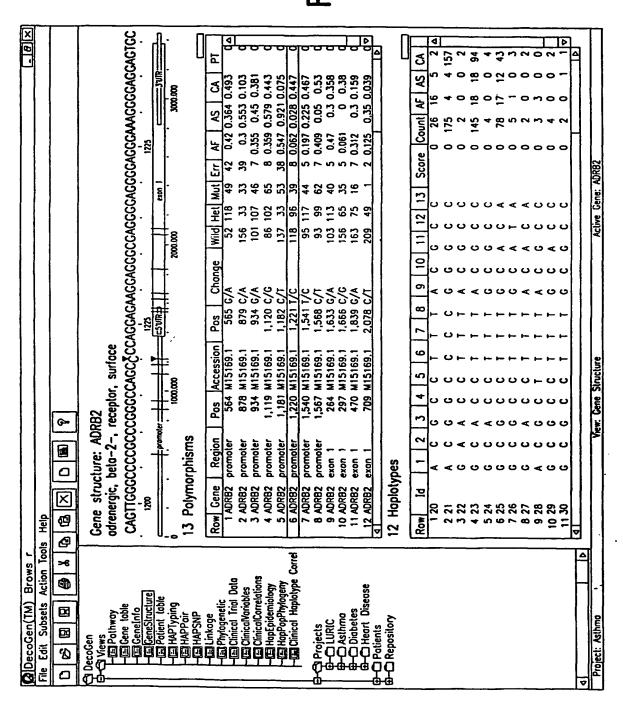
SUBSTITUTE SHEET (RULE 26)

FIG. 28A



SUBSTITUTE SHEET (RULE 26)

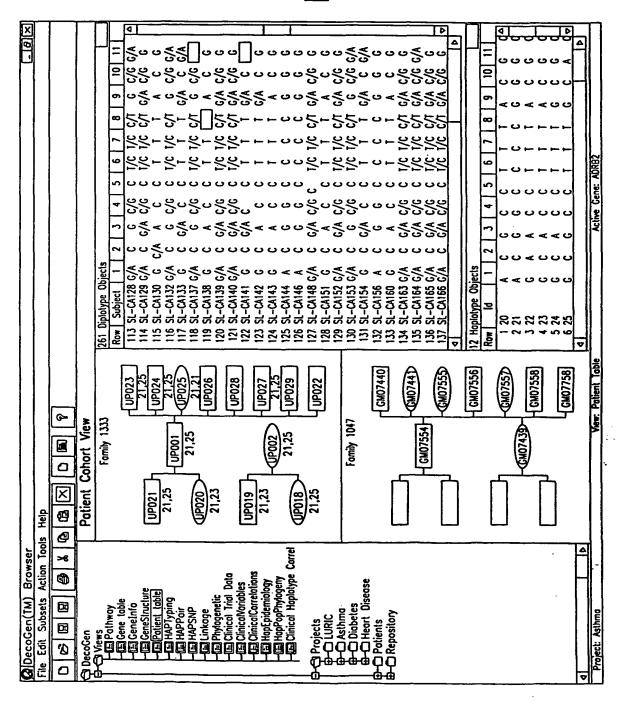
FIG. 28B



SUBSTITUTE SHEET (RULE 26)

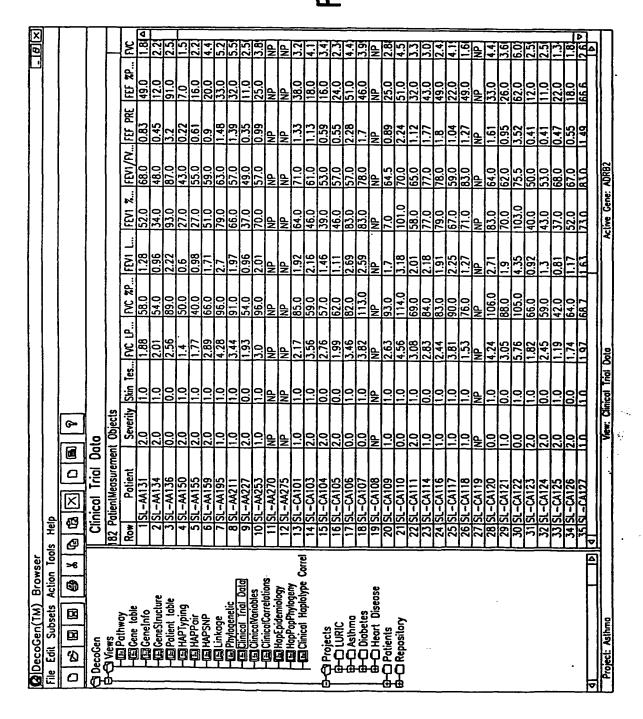
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FIG. 29A



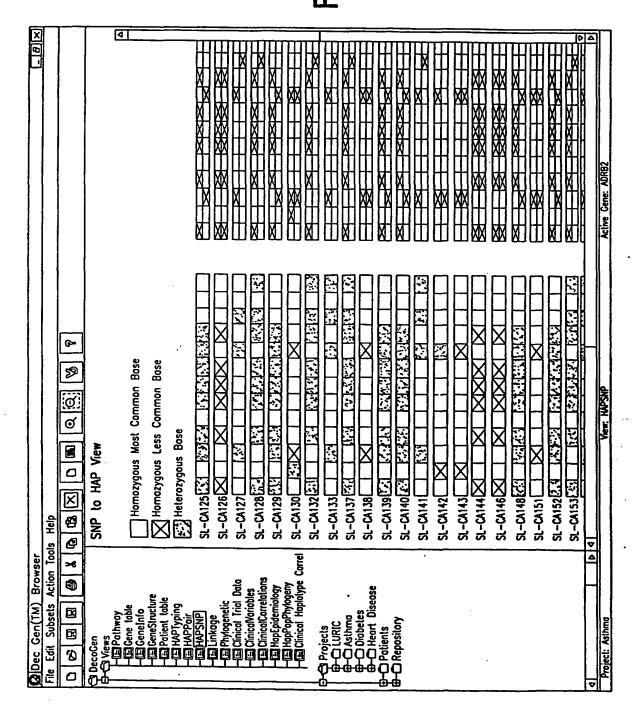
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-1G. **29E**



SUBSTITUTE SHEET (RULE 26)

FIG. 30



SUBSTITUTE SHEET (RULE 26)

-1G. 3

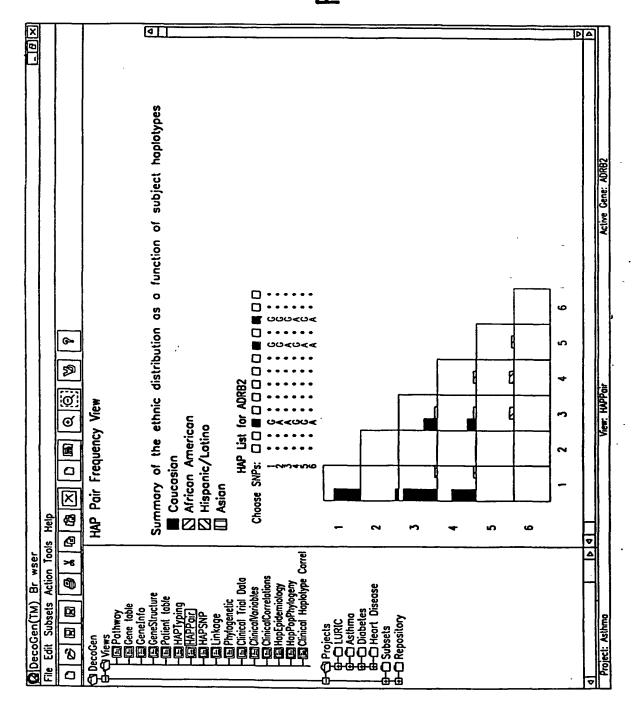


FIG. 32

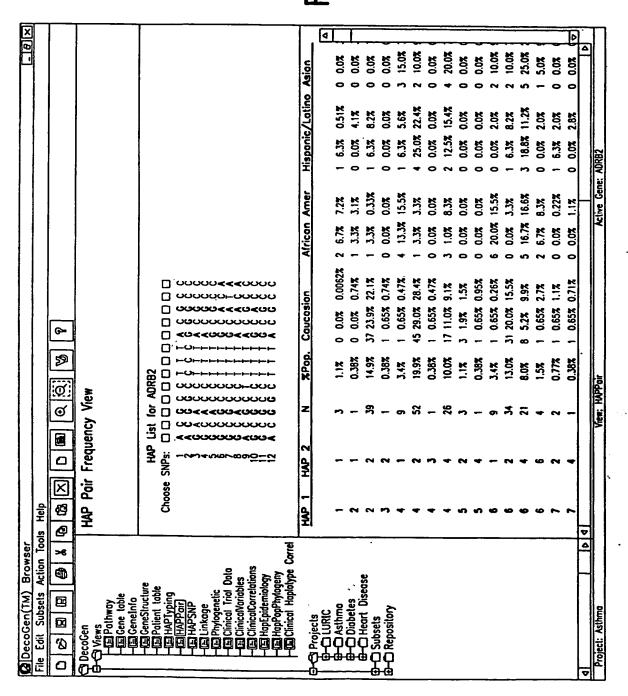
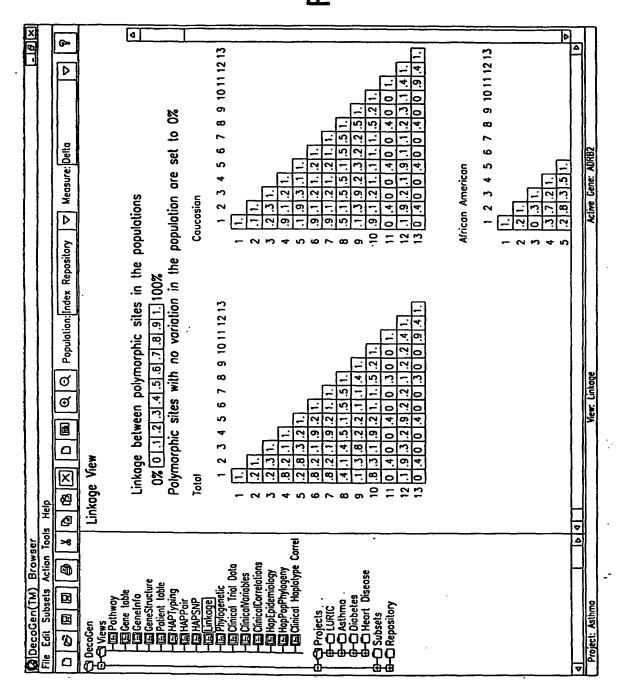
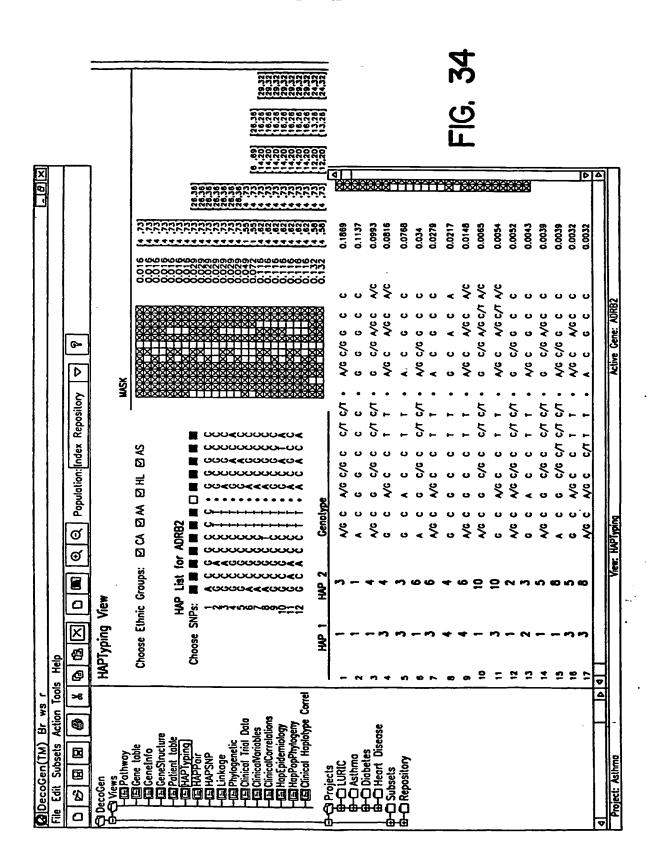


FIG. 3



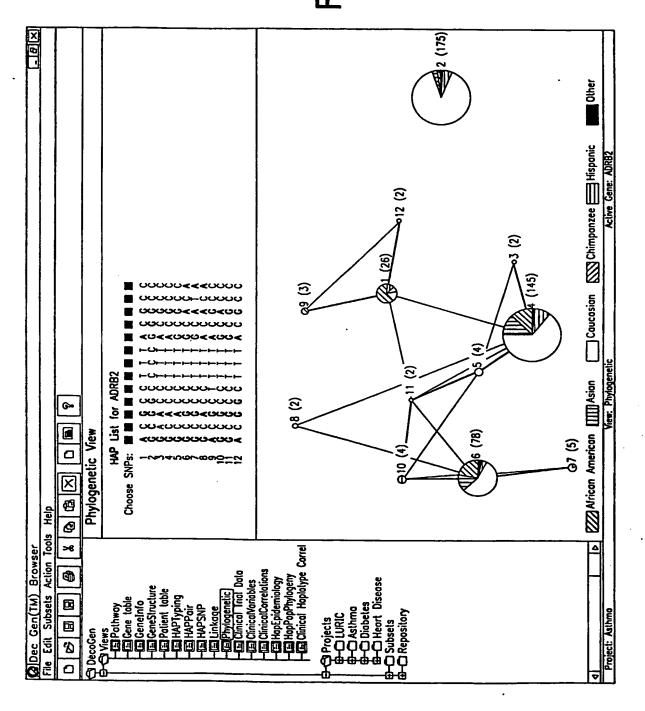
SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

FIG. 35



SUBSTITUTE SHEET (RULE 26)

FIG. 36

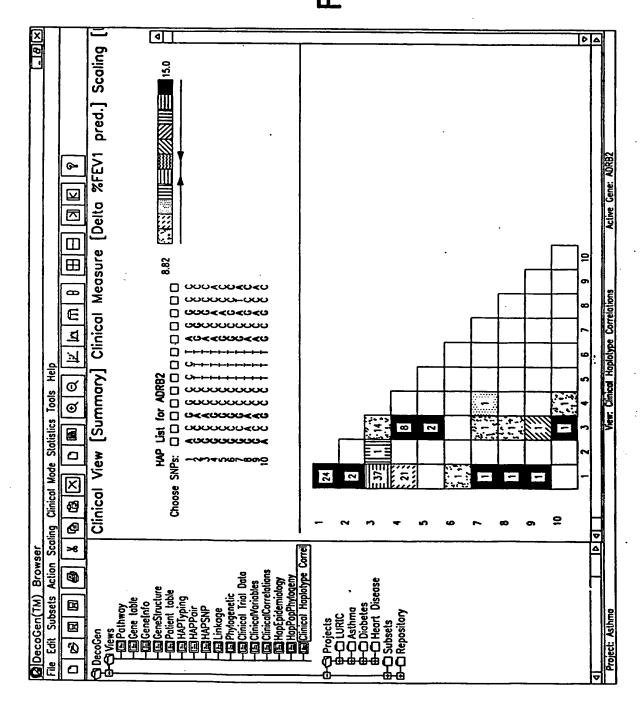
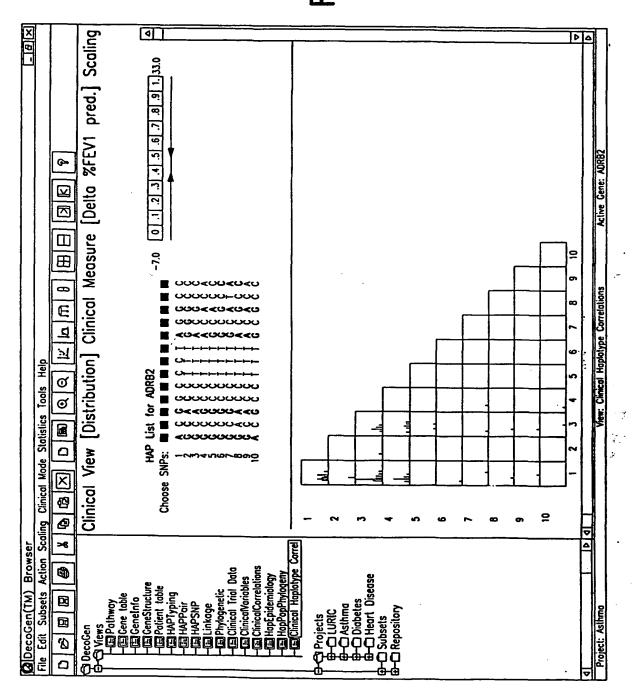


FIG. 37



SUBSTITUTE SHEET (RULE 26)

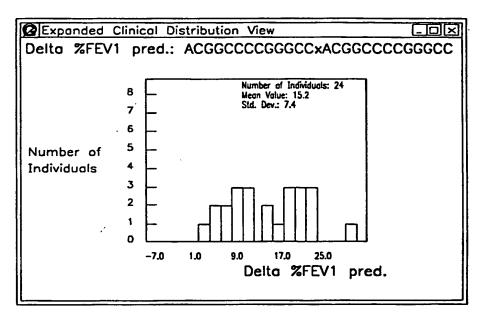


FIG. 38

DecoGen Single Gene	Statistics	Calculato	r					
File								
Show/Hide]	CC Line]						
Gene: odrenergic, b	eta-2-, 1	receptor.	surface			ure: Delta %	FEV1 pr	d.
			Confidence:	0.05 0.1	Fixed Si	te: -4		
								لے
Regression Resul	ts						_	
Marker	Intercept	Slope	Stope Ran	ige	R** 2	Corr. Coef (R)	P-value	
	10.501	1.99	-0.08	4.06	0.0301	0.1734	0.0297	
	10.526	1.956	-0.11	4.02	0.0293	0.1711	0.0314	<u> </u>
	14.583	-2.206	-4.28	-0.13	0.0365	-0.1911	0.0187	- 1
+A++++A+++	14.471	-2.04B	-4.13	0.032	0.0315	-0.1774	0.0268	- -
□**A*****G**	14.626	-2.241	-4.32	-0.16	0.0374	-0.1934	0.0175	ı
□++A+++++A+G++	14.615	-2.308	-4.4	-0.21	0.0391	-0.1977	0.0155	
GCACCTTTACGCC	14.6	-2.343	-4.46	-0.22	0.0394	-0.1984	0.0153	- 1
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FIG. 39A

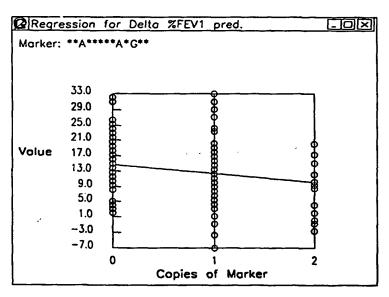
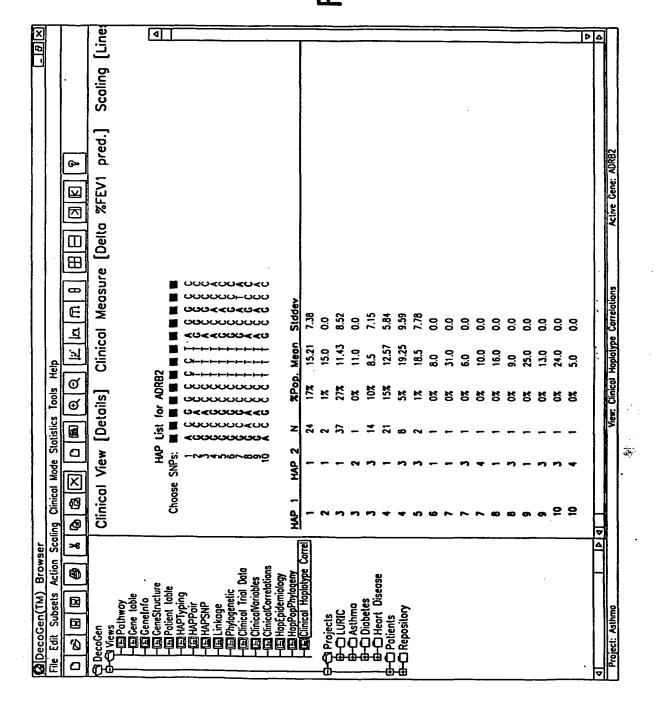


FIG. 39B

FIG. 40



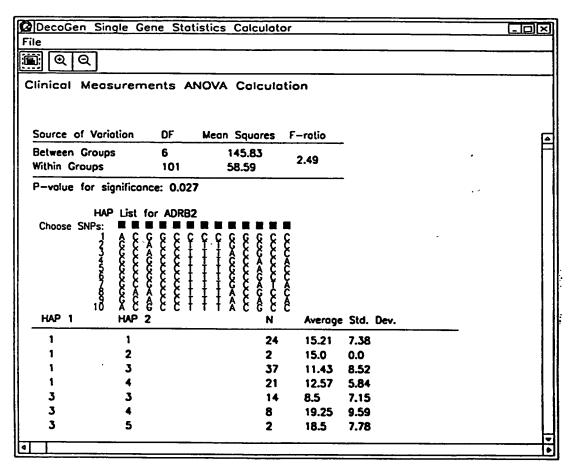
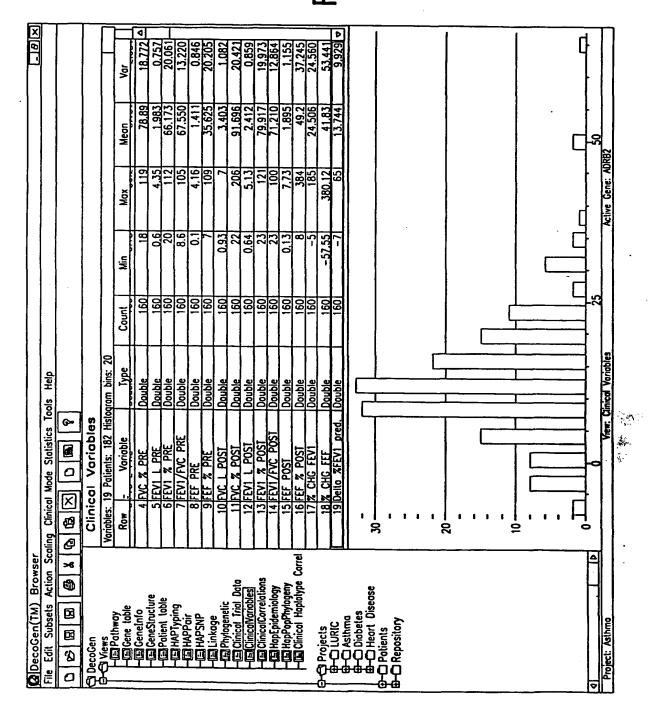


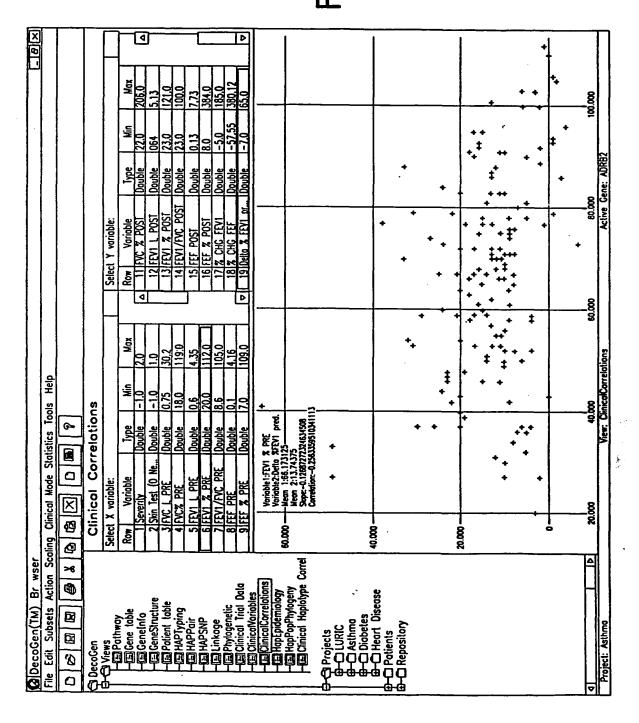
FIG. 41

FIG. 42

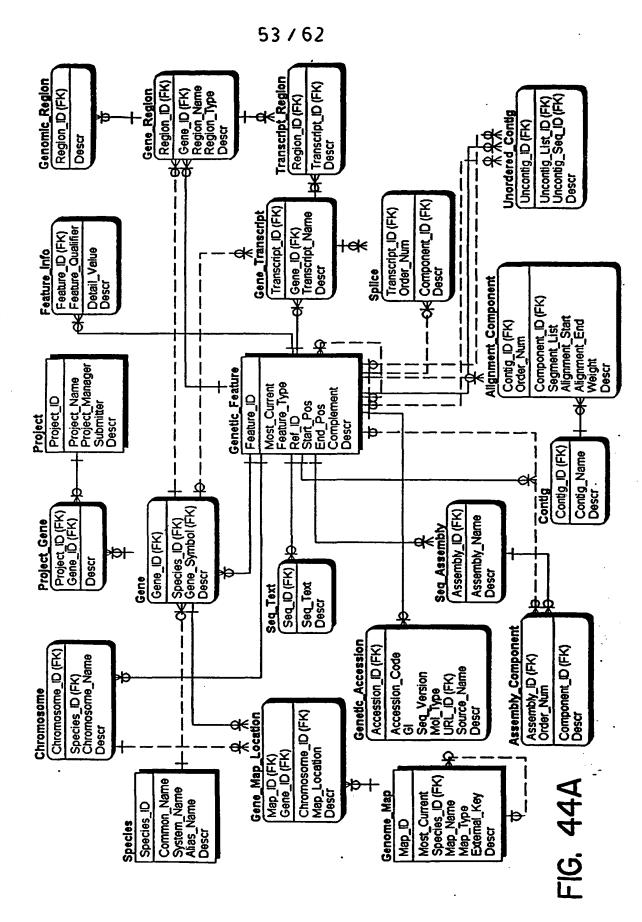


SUBSTITUTE SHEET (RULE 26)

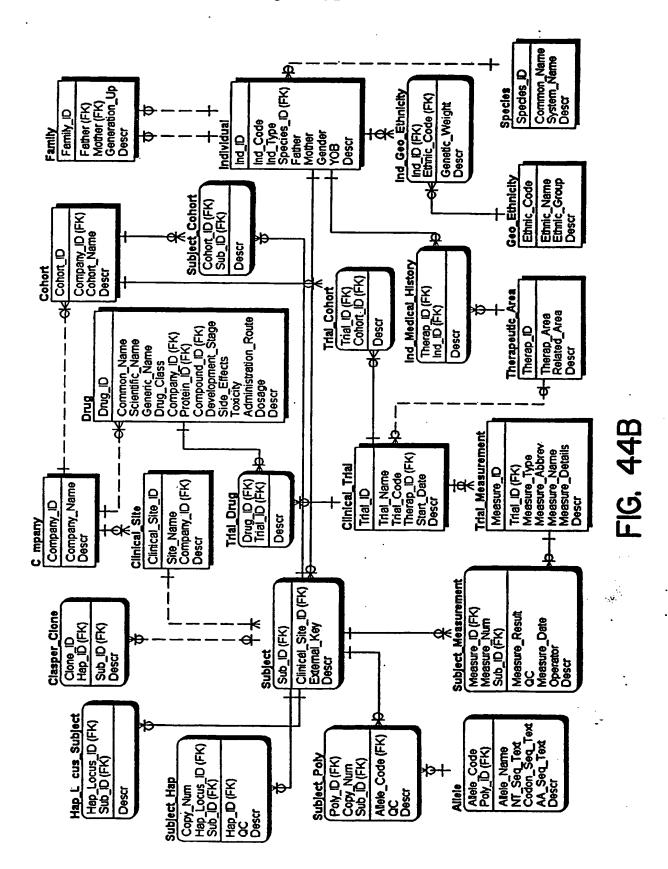
FIG. 45



SUBSTITUTE SHEET (RULE 26)

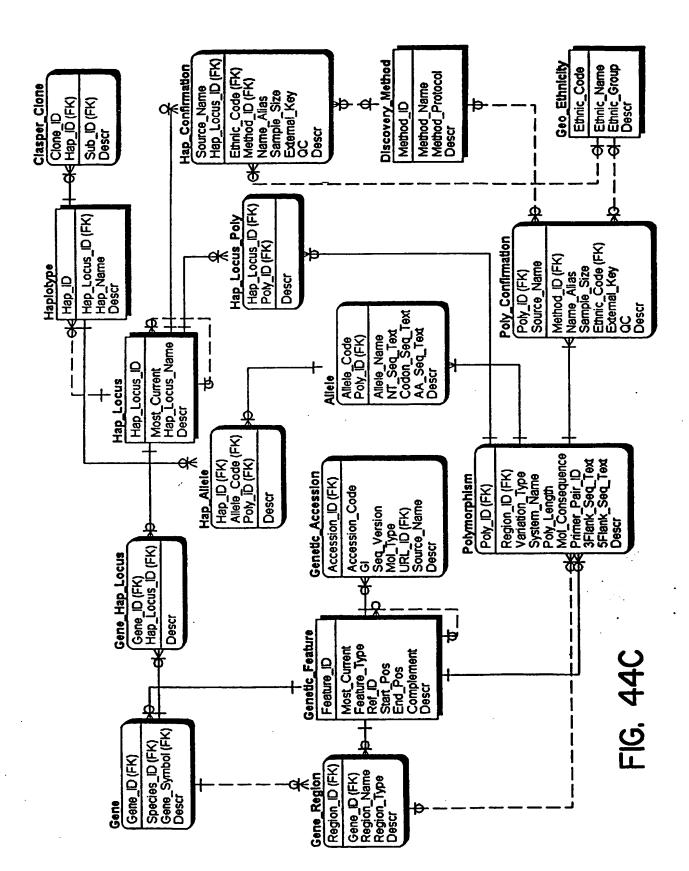


SUBSTITUTE SHEET (RULE 26)



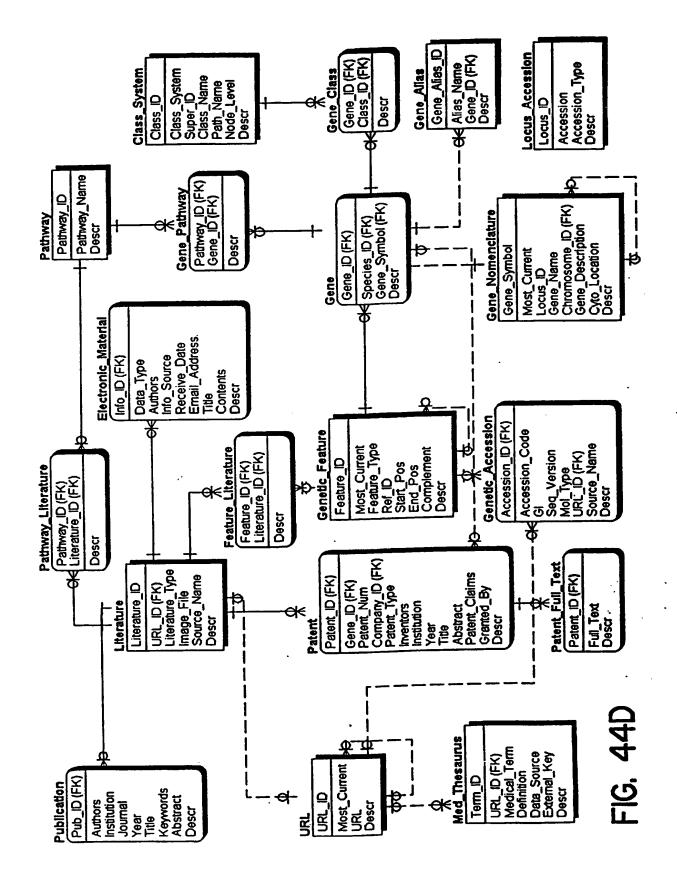
SUBSTITUTE SHEET (RULE 26)

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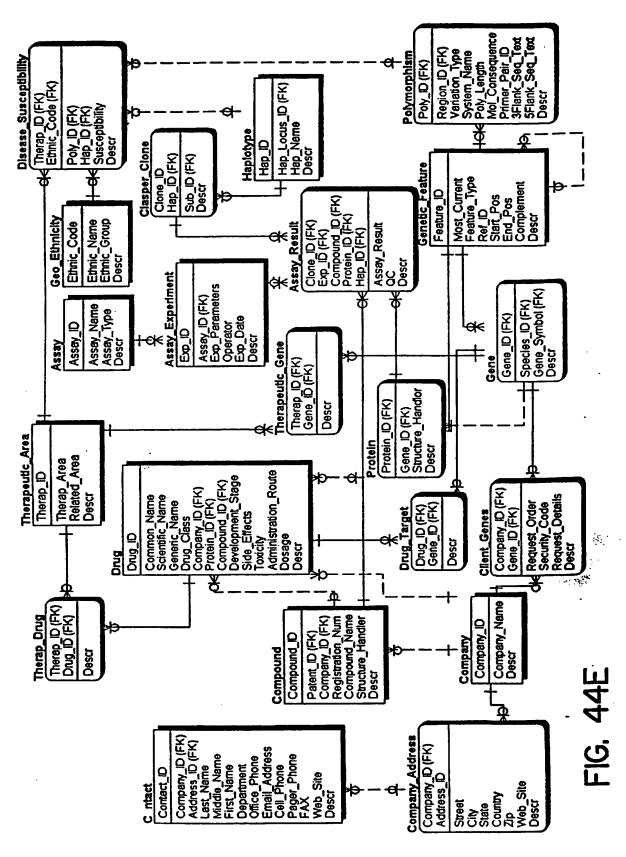
SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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Legend of Figures:



Rectangle Boxes: Tables in the database.

Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: | Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: P-- A Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.

- 10: | Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.

FIG. 44F

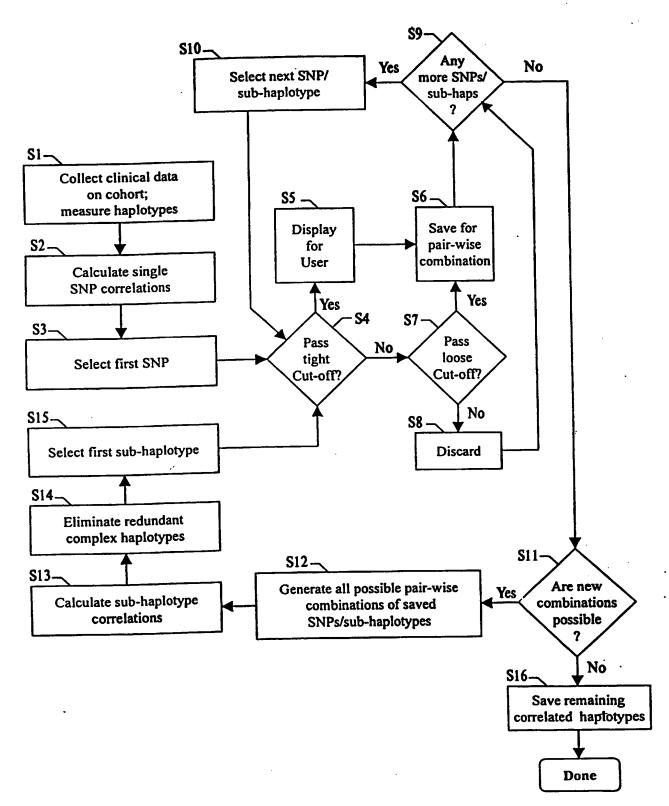


FIG. 45
SUBSTITUTE SHEET (RULE 26)

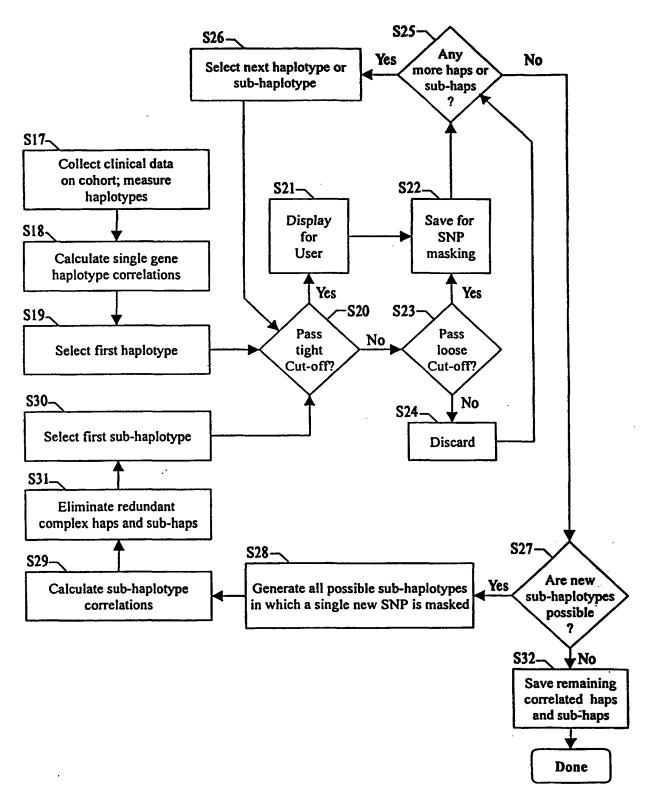


FIG. 46

SUBSTITUTE SHEET (RULE 26)

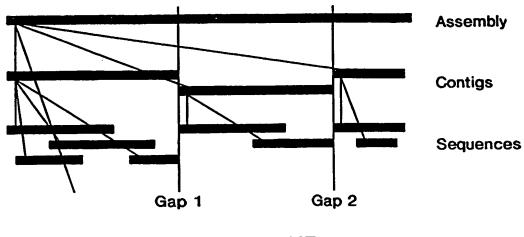


FIG. 47

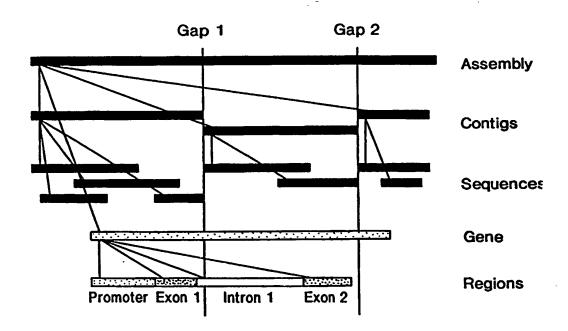


FIG. 48

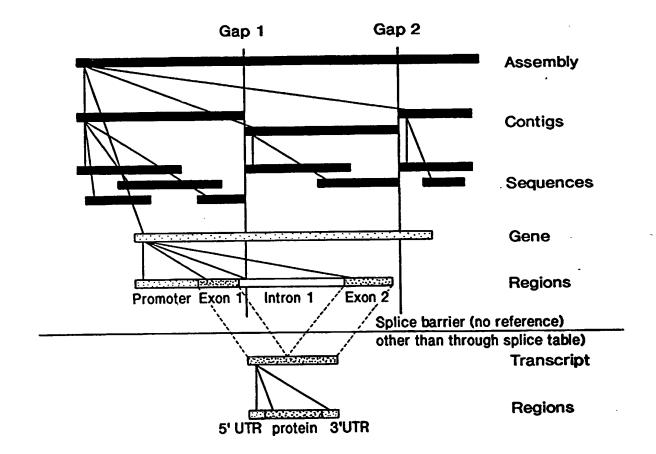


FIG. 49